USAF School of Aerospace Medicine & Defense Health Agency

DoD Global, Laboratory-Based, Influenza Surveillance Program

2016-2017

Cumulative Results

Locations	79
Collected	2,971
Tested	2,774

Influenza A	**833**
A(H1N1)pdm09	6
A(H3N2)	825
A(H3N2) & RSV	1
A/not subtyped & rhino/enterovirus	1

Influenza B*	**73**
B	72
B & Human Metapneumovirus &	1

Other Respiratory Pathogens	**723**
Adenovirus	45
Bordetella pertussis	0
Chlamydophila pneumoniae	2
Coronavirus	83
Human Metapneumovirus	38
Mycoplasma pneumoniae	30
Parainfluenza	120
RSV	132
Rhino/Enterovirus	182
Non-influenza Viral Coinfections	83
Non-influenza Bacterial Coinfections	8
-*M. pneumo* coinfections (8)	

Results are preliminary and may change as more results are finalized.
**Influenza B lineages will be reported in the periodic molecular sequencing reports.*

Respiratory Highlights
5 - 18 February 2017 (Surveillance Weeks 6 & 7)

- During 5 - 18 February 2017, a total of 608 specimens were collected from 46 locations. Results were finalized for 455 specimens from 44 locations. During Week 6, one influenza A(H1N1)pdm09, 139 influenza A(H3N2) and 16 influenza B viruses were identified. During Week 7, one influenza A(H1N1)pdm09, 109 influenza A(H3N2) and 14 influenza B viruses were identified. Approximately 46% of specimens tested positive for influenza during Week 6. Approximately 47% of specimens tested positive for influenza during Week 7. The influenza percent positive for the season is approximately 33%.

- According to WHO, influenza activity continues to be elevated worldwide with influenza A(H3N2) virus dominating. This increasing trend can still be seen in the United States and Mexico. In contrast, Canada, East Asia, Northern Africa, and Europe are reporting decreasing trends as compared to previous weeks. The majority of collected viruses tested for antiviral sensitivity were found to be susceptible to neuraminidase inhibitor antiviral medications. Additionally, most samples contained viruses that are antigenically matched to the reference strains used in the 2016-17 influenza vaccine (WHO Influenza Update, cited 23 February 2017).

- As of last week, the US Centers for Disease Control and Prevention reported that the interim influenza vaccine effectiveness estimate was approximately 48%. The European Centre for Disease Prevention had similar findings (CIDRAP, cited 23 February 2017).

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Table 1. Results by region and location for specimens collected during Weeks 6 & 7

Region*		A(H1N1)pdm09	A(H3N2)	B	Adenovirus	Coronavirus	hMNV	*M. pneumoniae*	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & Corona	Adeno & RSV	Adeno & RSV & Rhino/Entero	Adeno & Rhino/Entero	Corona & RSV	Corona & Rhino/Entero	RSV & Rhino/Entero	No Pathogen	Total
Deployed	Country 2, Location A	-	1	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	3
PACOM	Kadena AB, Japan	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	1
	Yokota AB, Japan	-	8	1	-	-	-	-	-	-	-	-	-	-	-	-	1	-	1	11
Region 1	Hanscom AFB, MA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	USCG Academy, CT	-	5	1	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	7
Region 2	Ft Drum, NY	-	5	5	-	-	1	-	-	2	-	-	-	-	-	-	-	-	4	17
	JB McGuire-Dix-Lakehurst, NJ	-	5	-	-	1	2	-	-	-	-	-	-	-	-	-	-	-	3	11
	USMA - West Point, NY	-	32	2	-	1	-	-	-	1	2	-	-	-	-	-	-	-	8	46
Region 3	Dover AFB, DE	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	6
	JB Anacostia-Bolling, DC	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3
	JB Andrews, MD	-	6	-	-	-	1	-	1	-	-	-	-	-	-	-	-	-	5	13
	JB Langley-Eustis, VA	-	44	1	-	1	-	-	-	2	3	-	-	-	-	-	-	-	13	64
Region 4	Columbus AFB, MS	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	2
	Eglin AFB, FL	-	2	-	-	-	-	1	-	1	-	-	-	-	-	-	-	-	3	7
	Ft Bragg, NC	1	2	1	-	-	-	-	-	-	-	1	-	-	-	-	-	-	2	7
	Hurlburt Field, FL	-	2	-	1	-	-	1	-	-	-	-	-	-	-	-	-	-	1	5
	JB Charleston (AF), SC	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	Maxwell AFB, AL	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Moody AFB, GA	-	3	1	-	-	1	-	1	1	-	-	-	-	-	-	-	-	-	7
	Robins AFB, GA	-	3	2	-	-	-	1	-	1	1	-	-	-	-	-	-	-	4	12
	Seymour Johnson AFB, NC	1	4	1	1	-	-	-	-	1	-	-	-	-	-	-	-	-	3	11
	Shaw AFB, SC	-	2	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6

(Cont'd on page 3)

**CONUS locations are based on Health & Human Services regions. Other locations are defined by COCOM.*

Table 1. Results by region and location for specimens collected during Weeks 6 & 7

(Cont'd from page 2)

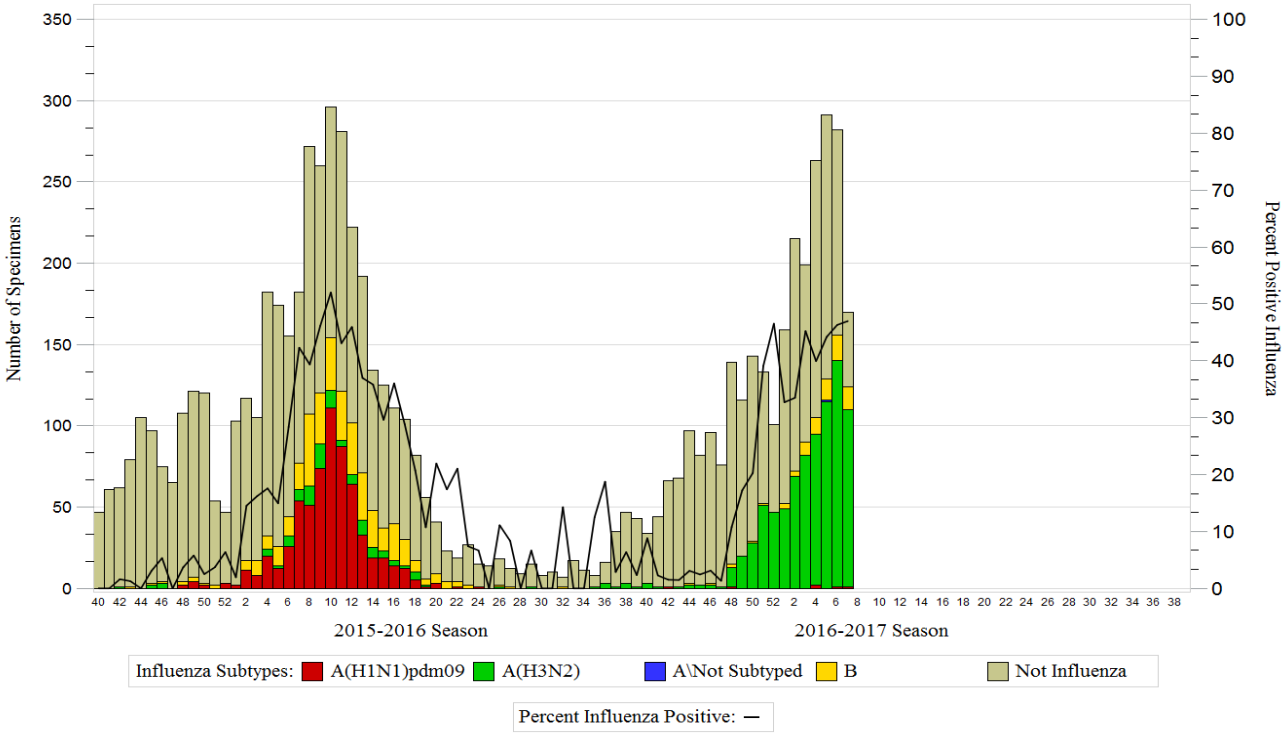
Region 5	Wright-Patterson AFB, OH	-	2	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	7
Region 6	Altus AFB, OK	-	1	-	-	1	-	-	-	1	1	-	-	-	-	1	-	-	4	9
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Cannon AFB, NM	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4
	Laughlin AFB, TX	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Little Rock AFB, AR	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3
	Sheppard AFB, TX	-	16	-	-	3	-	-	-	-	-	-	-	-	-	-	-	-	8	27
	Tinker AFB, OK	-	32	5	-	2	-	-	-	1	-	1	-	-	-	-	-	1	11	53
Region 7	McConnell AFB, KS	-	11	-	-	1	-	-	1	-	1	-	-	-	-	-	-	-	-	14
	Offutt AFB, NE	-	9	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	2	12
Region 8	Ellsworth AFB, SD	-	2	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	2	5
	FE Warren AFB, WY	-	7	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	5	13
	Hill AFB, UT	-	2	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	4
	Malmstrom AFB, MT	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	Minot AFB, ND	-	10	2	-	-	-	-	-	1	-	-	1	-	-	-	-	-	5	19
	Peterson AFB, CO	-	6	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	2	10
Region 9	Davis-Monthan AFB, AZ	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1
	Luke AFB, AZ	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1
	Nellis AFB, NV	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Travis AFB, CA	-	3	-	-	2	-	-	-	3	2	-	-	1	-	-	-	1	3	15
Region 10	Fairchild AFB, WA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Mt Home AFB, ID	-	3	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	1	6
Total		2	248	30	3	15	6	3	3	21	12	2	1	1	1	1	1	2	100	452

**CONUS locations are based on Health & Human Services regions. Other locations are defined by COCOM.*

DoD Global, Laboratory-Based, Influenza Surveillance Program

Laboratory Results - Cumulative for Season

Graph 1. Percent influenza positive by week: 2015-2016 surveillance year and through Week 7 of the 2016-2017 surveillance year



Note: Dual influenza coinfections are excluded from this graph. Specimens with pending results are used in the denominator to calculate percent

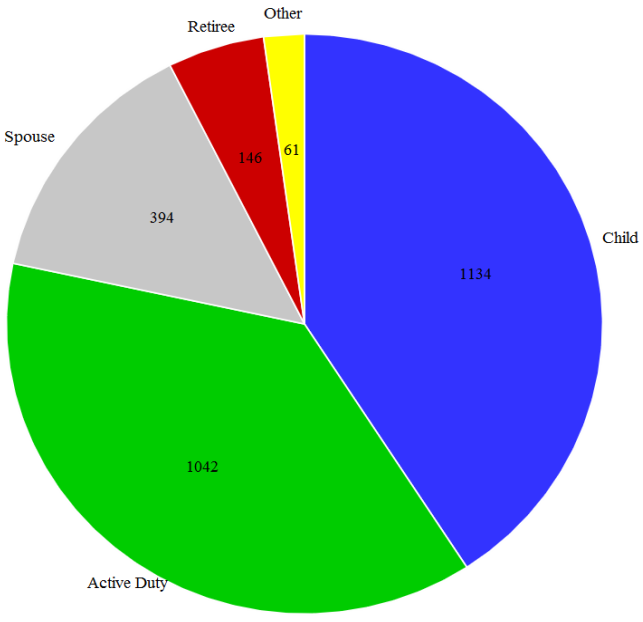
Table 2. ILI by age group for the 2016-2017 surveillance year through Week 7

Age Group	Frequency	Percent
0-5	620	22.33
6-9	203	7.31
10-17	312	11.24
18-24	435	15.66
25-44	880	31.69
45-64	260	9.36
65+	67	2.41

Demographic Summary

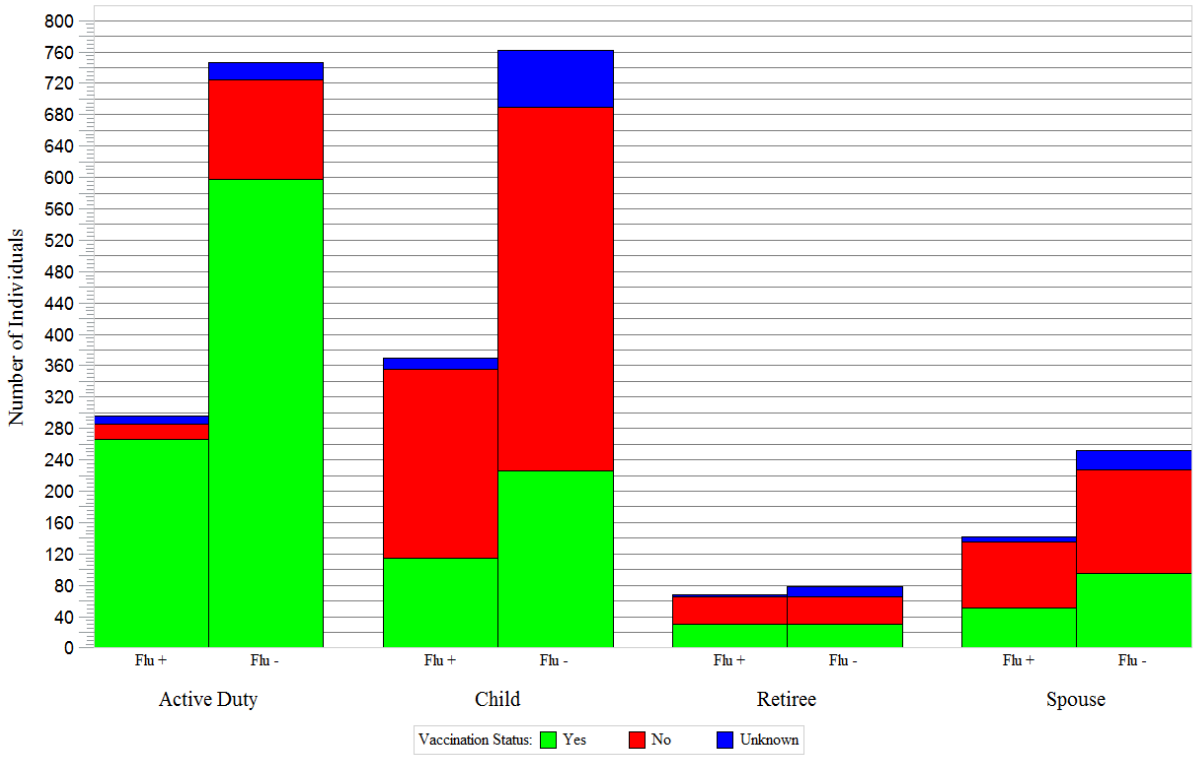
Of 2,777 ILI cases, 1,042 (37.5%) are service members, 1,134 (40.8%) are children, 394 (14.2%) are spouses, and 207 (7.5%) are retirees and other beneficiaries. The median age of ILI cases with known age (n=2,777) is 22 (range 0, 96).

Graph 2. ILI by beneficiary status for the 2016-2017 surveillance year through Week 7

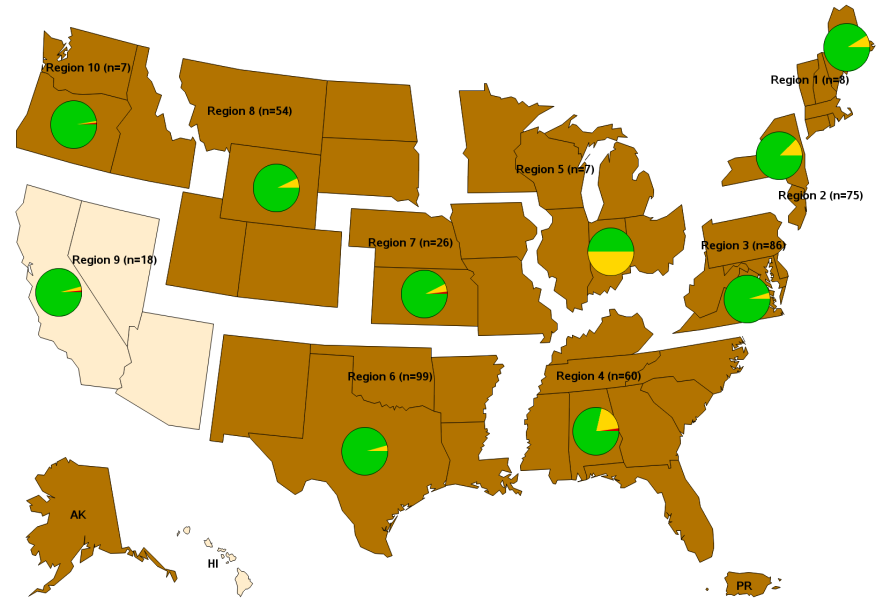


88ABW-2015-5508 and PA email guidance dated 10 November 2015.

Graph 3. Vaccination status by beneficiary type for the 2016-2017 surveillance year through Week 7



Map 1. Influenza subtypes and activity level by U.S. region for the 2016-2017 surveillance year through Week 7



HI - Region 9

AK - Region 10

PR - Region 2

Influenza Activity - Past 2 weeks

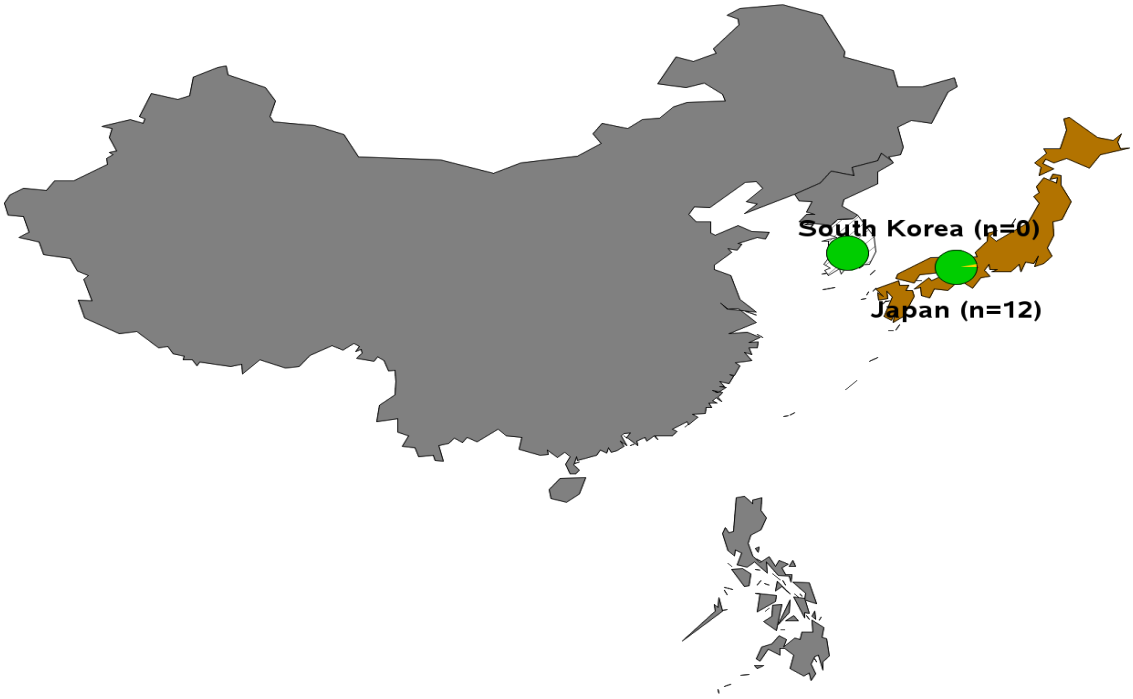
(n = # of finalized results)

- No activity (0% +) or no submissions
- Low (<25% +)
- Moderate (25-49% +)
- High (>50% +)

Influenza Results - Cumulative

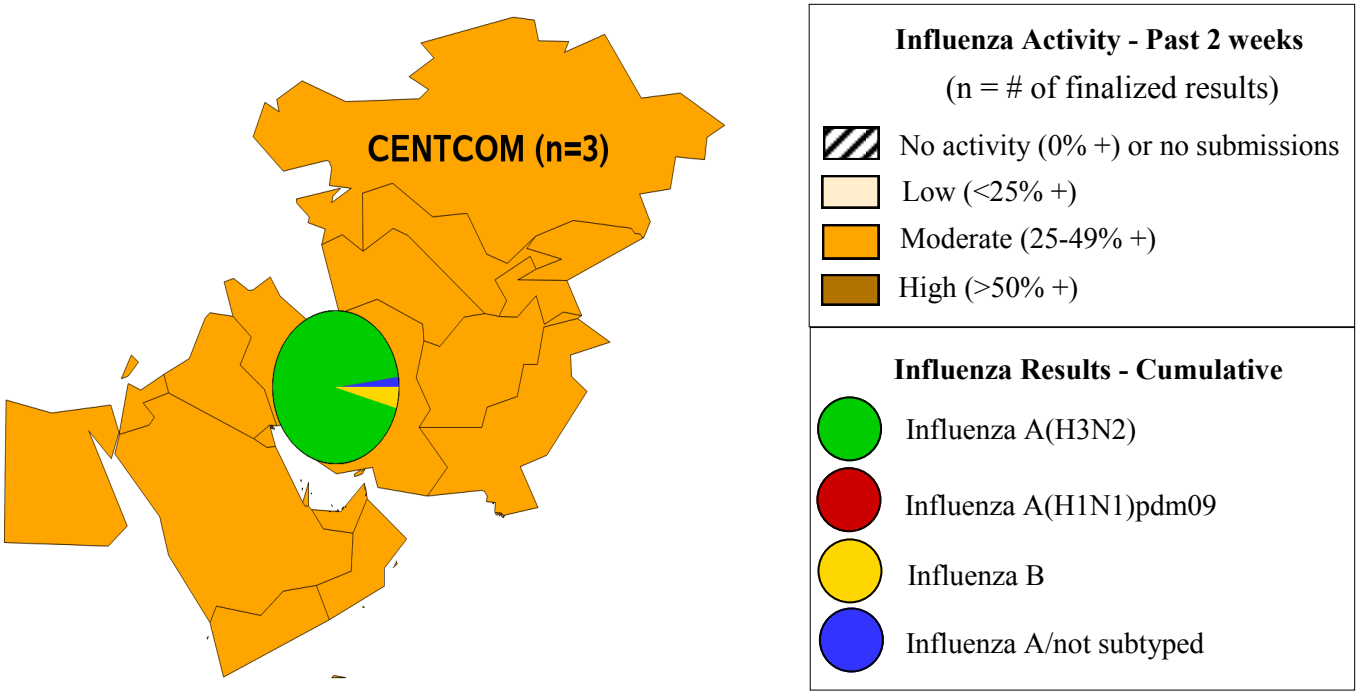
- Influenza A(H3N2)
- Influenza A(H1N1)pdm09
- Influenza B
- Influenza A/not subtyped

Map 2. Influenza subtypes and activity level by country for the 2016-2017 surveillance year through Week 7 (Pacific)



Note - Countries shaded in gray do not contain sentinel sites and are only displayed for geographical perspective.

Map 3. Influenza subtypes and activity level for CENTCOM for the 2016-2017 surveillance year through Week 7



Note - Specimens for CENTCOM were tested at USAFSAM or Landstuhl Regional Medical Center (LRMC).

Laboratory Results—Through Current Surveillance Week 7

Table 3. Cumulative results by region and location for specimens collected during the 2016-2017 surveillance year

Region*		A(H1N1)pdm09	A(H3N2)	A/not subtyped & Rhino/Entero	A(H3N2) & RSV	B	B & hMNV & Rhino/Entero	Adenovirus	*C. pneumoniae*	Coronavirus	hMNV	*M. pneumoniae*	Parainfluenza	RSV	Rhinovirus/Enterovirus	Non-Influenza Viral Coinfection	Non-Influenza Bacterial Coinfection	No Pathogen	Total
Deployed	Country 1, Location A	-	3	-	-	-	-	-	-	1	-	-	-	1	-	-	-	7	12
	Country 1, Location B	-	6	-	-	1	-	-	-	1	-	-	-	1	-	1	-	5	15
	Country 1, Location D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Country 2, Location A	-	30	1	-	1	-	-	-	6	-	-	-	-	6	2	-	11	57
EUCOM	Incirlik AB, Turkey	-	1	-	-	1	-	-	-	-	-	-	-	-	-	-	-	1	3
PACOM	CFA Okinawa, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Eielson AFB, AK	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	5	6
	JB Elmendorf-Richardson, AK	-	1	-	-	-	-	-	-	-	-	-	-	-	1	-	-	3	5
	JR Marianas - Andersen AFB, Guam	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	2
	Kadena AB, Japan	-	4	-	-	-	-	-	-	-	1	-	3	-	2	-	1	19	30
	Kunsan AB, South Korea	-	2	-	-	-	-	-	-	1	-	-	-	-	1	-	-	1	5
	Misawa AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Osan AB, South Korea	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7	10
	Tripler AMC, HI	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Yokota AB, Japan	-	26	-	-	1	-	1	-	3	1	2	-	2	7	4	-	48	95
Region 1	Hanscom AFB, MA	-	2	-	-	-	-	-	-	-	-	1	2	-	-	1	-	2	8
	USCG Academy, CT	-	9	-	-	1	-	-	-	1	1	1	-	-	3	-	2	5	23
Region 2	CGAS Borinquen, PR	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Ft Drum, NY	-	7	-	-	14	-	5	-	1	8	1	6	7	1	2	-	18	70
	JB McGuire-Dix-Lakehurst, NJ	-	35	-	-	-	-	2	-	6	5	2	7	5	9	4	-	58	133
	USMA - West Point, NY	-	77	-	-	3	-	10	-	5	3	1	5	10	6	4	-	94	218
Region 3	Dover AFB, DE	-	9	-	-	-	-	1	-	1	-	1	-	1	1	-	-	25	39
	JB Anacostia-Bolling, DC	-	5	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	6
	JB Andrews, MD	-	16	-	-	1	-	-	-	1	1	-	1	2	1	2	-	26	51
	JB Langley-Eustis, VA	-	56	-	-	3	-	-	-	3	3	2	4	19	25	8	-	79	202
	NMC Portsmouth, VA	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	2	3
	US Naval Academy, MD	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Region 4	Columbus AFB, MS	-	3	-	-	1	-	-	-	1	-	-	-	-	1	-	-	11	17
	Eglin AFB, FL	-	10	-	-	1	-	2	-	1	-	1	-	5	9	3	-	20	52
	Ft Bragg, NC	1	6	-	-	4	-	-	-	1	-	1	3	2	6	4	3	24	55
	Ft Campbell, KY	1	15	-	-	2	1	2	-	-	1	-	-	3	-	4	-	11	40
	Hurlburt Field, FL	-	9	-	-	-	-	1	-	-	-	1	1	-	-	-	-	9	21
	JB Charleston (AF), SC	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	7
	Keesler AFB, MS	-	-	-	-	-	-	-	-	-	-	-	1	2	1	1	-	8	13
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	3	4
	Maxwell AFB, AL	-	3	-	-	-	-	-	-	-	-	-	1	-	1	-	-	8	13
	Moody AFB, GA	-	16	-	-	3	-	1	-	1	1	-	3	6	4	8	1	23	67
	NH Beaufort, SC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	NH Camp Lejeune, NC	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5	6
	NH Jacksonville, FL	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	3
	Patrick AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Robins AFB, GA	-	15	-	-	4	-	-	-	-	-	2	-	2	1	-	-	12	36
	Seymour Johnson AFB, NC	1	7	-	-	1	-	2	-	-	-	1	1	1	1	-	-	7	22
	Shaw AFB, SC	-	13	-	-	8	-	1	-	5	1	1	3	1	3	-	-	27	63
Region 5	Scott AFB, IL	-	-	-	-	1	-	-	-	-	-	1	2	1	1	-	1	7	14
	Wright-Patterson AFB, OH	-	3	-	-	2	-	-	-	-	-	1	1	-	1	2	-	15	25

(Cont'd on page 8)

**CONUS locations are based on Health & Human Services regions. Other locations are defined by COCOM.*

Laboratory Results—Through Current Surveillance Week 7

Table 3. Cumulative results by region and location for specimens collected during the 2016-2017 surveillance year *(Cont'd from page 7)*

Region 6	Altus AFB, OK	-	5	-	-	-	-	1	-	1	1	-	-	5	5	3	-	29	50
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	-	-	2	-	1	-	-	5	8
	Cannon AFB, NM	-	6	-	-	-	-	-	-	1	-	1	1	-	3	-	-	14	26
	Ft Polk, LA	-	1	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	3
	JBSA Lackland, TX	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	1
	Laughlin AFB, TX	-	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	2	4
	Little Rock AFB, AR	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	7
	Sheppard AFB, TX	-	50	-	-	-	-	-	-	7	2	-	6	-	6	-	-	48	119
	Tinker AFB, OK	-	70	-	1	6	-	2	-	7	-	1	5	5	6	2	-	69	174
	Vance AFB, OK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	12	12
Region 7	McConnell AFB, KS	-	21	-	-	-	-	-	-	4	-	1	3	1	5	-	-	17	52
	Offutt AFB, NE	1	30	-	-	3	-	1	-	3	-	-	1	1	5	1	-	28	74
Region 8	Ellsworth AFB, SD	-	11	-	-	-	-	-	-	3	-	-	3	-	3	-	-	20	40
	FE Warren AFB, WY	-	24	-	-	1	-	2	-	3	-	1	2	5	3	-	-	25	66
	Hill AFB, UT	-	23	-	-	1	-	-	-	2	-	-	4	3	4	-	-	26	63
	Malmstrom AFB, MT	-	7	-	-	1	-	-	-	-	-	1	-	-	1	-	-	4	14
	Minot AFB, ND	-	15	-	-	2	-	-	-	1	1	1	-	2	2	2	-	12	38
	Peterson AFB, CO	-	16	-	-	2	-	-	-	2	-	-	1	8	3	4	-	15	51
	USAF Academy, CO	-	1	-	-	-	-	-	-	-	1	-	-	1	1	-	-	2	6
Region 9	Beale AFB, CA	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5
	Davis-Monthan AFB, AZ	-	7	-	-	-	-	-	-	-	-	-	5	-	4	5	-	18	39
	Edwards AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Luke AFB, AZ	-	-	-	-	-	-	-	-	2	-	-	-	2	-	1	-	4	9
	Nellis AFB, NV	1	3	-	-	2	-	3	-	1	-	-	4	3	5	6	-	16	44
	Travis AFB, CA	-	53	-	-	-	-	-	1	3	4	-	6	8	11	3	-	32	121
	Vandenberg AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
Region 10	CGS North Bend, OR	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4
	Fairchild AFB, WA	1	14	-	-	1	-	2	-	3	-	-	4	2	4	-	-	38	69
	JB Lewis-McChord, WA	-	2	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	3
	Mt Home AFB, ID	-	22	-	-	-	-	1	1	1	-	1	23	10	12	4	-	64	139
	NH Bremerton, WA	-	33	-	-	-	-	4	-	-	-	-	6	4	4	2	-	14	67
Total		6	825	1	1	72	1	45	2	83	38	30	120	132	182	83	8	1145	2774

**CONUS locations are based on Health & Human Services regions. Other locations are defined by COCOM.*

Molecular Sequence Analysis Report #4

USAFSAM Epidemiology Laboratory Service

This is the fourth USAFSAM influenza sequence surveillance report for the 2016-2017 influenza season and includes a total of 61 specimens collected between 1 August 2016 and 18 January 2017, with 35 specimens sequenced at USAFSAM, 17 hemagglutinin sequences provided by the Naval Medical Research Unit 2 (NAMRU-2) in Cambodia, and nine hemagglutinin sequences provided by the United States Army Medical Research Unit in Kenya (USAMRU-K). Among the specimens analyzed, five (8.2%) were influenza A(H1N1)pdm09, 38 (62.3%) were influenza A(H3N2), 17 (27.9%) were influenza B/Victoria lineage, and one (1.6%) was influenza B/Yamagata lineage. Figure 1 shows the proportion of hemagglutinin (HA) sequences sequenced at USAFSAM and partner labs and analyzed for this report by subtype or lineage, and Figure 2 shows the proportions of subtype and lineage submitted by USMAJCOM. The number of sequences for each subtype and lineage included in this report are shown for each sentinel site and partner lab location in Table 1. Figures 3-6 display the phylogenetic relationships among HA sequences for influenza A(H1N1)pdm09, A(H3N2), and influenza B/Victoria and B/Yamagata lineages, respectively.

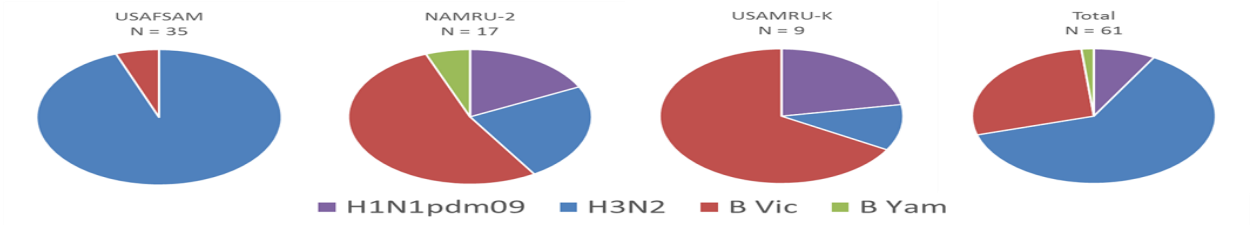


Figure 1: Proportion of hemagglutinin (HA) sequence subtypes and lineages analyzed for this report, sequenced at A) the United States School of Aerospace Medicine (USAFSAM), B) the Navy Medical Research Unit 2 (NAMRU-2), C) the United States Army Medical Research Unit in Kenya (USAMRU-K), and D) total laboratories

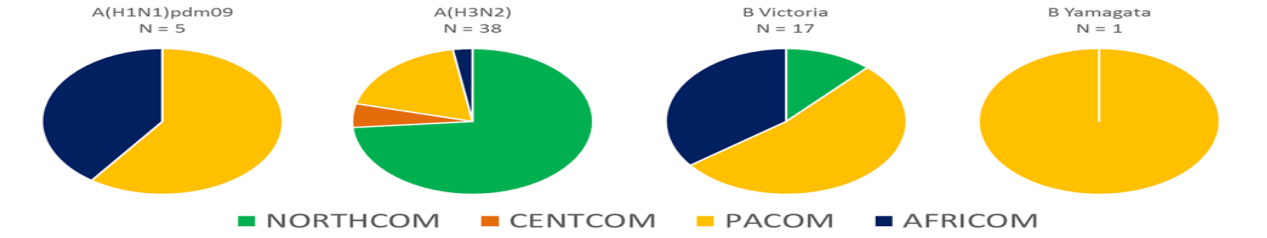


Figure 2: Proportion of HA sequences from each United States Major Command by A) influenza A(H1N1)pdm09, B) influenza A(H3N2), C) influenza B/Victoria, and D) influenza B/Yamagata. All sequences from AFRICOM were submitted by USAMRU-K, and the majority of sequences from PACOM were submitted by NAMRU-2.

Table 1: Influenza subtypes and lineages from corresponding sentinel sites and data from contributing labs included in the analyses for this report.

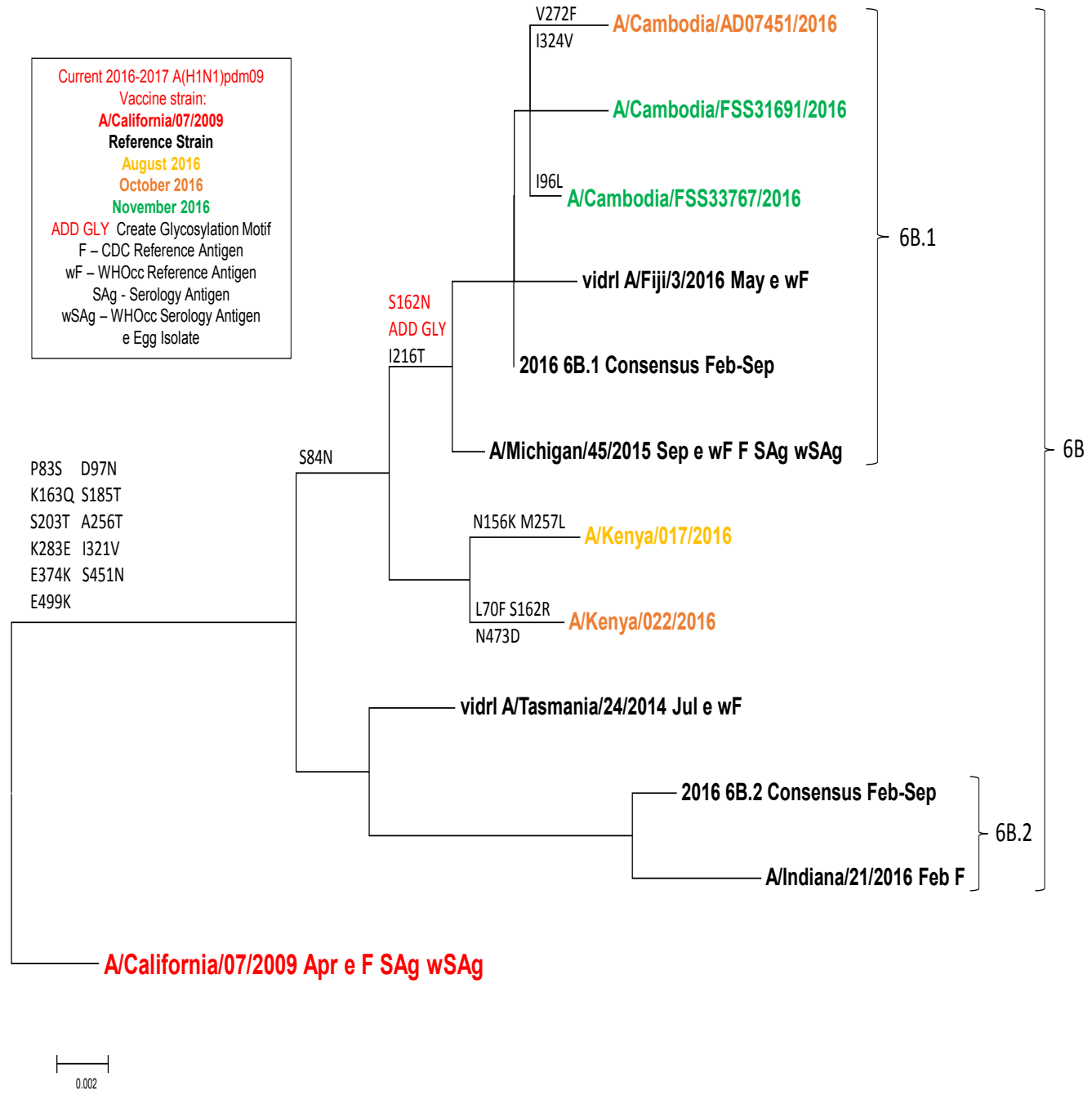
	A(H1N1)pdm09	A(H3N2)	B/Victoria	B/Yamagata	Grand Total
CONUS					
Alabama					
Maxwell AFB		1			1
Alaska					
Elmendorf AFB		1			1
Arizona					
Davis-Monthan AFB		1			1
California					
Travis AFB		2			2
Colorado					
Peterson AFB		1			1
Delaware					
Dover AFB		1			1
Kansas					
McConnell AFB		1			1
Kentucky					
Ft Campbell		2			2
Montana					
Malmstrom AFB		1			1
Nebraska					
Offutt AFB		1			1
(duplicate header)	A(H1N1)pdm09	A(H3N2)	B/Victoria	B/Yamagata	Grand Total
New Jersey					
JB McGuire-Dix-Lakehurst		1			1
New York					
Ft Drum		1			1
North Carolina					
Ft Bragg		1	2		3
Ohio					
Wright-Patterson AFB		2			2
Oklahoma					
Tinker AFB		1			1
Oregon					
CGS North Bend		1			1
South Carolina					
Shaw AFB		1			1
Texas					
Sheppard AFB		2			2
Utah					
Hill AFB		3			3
Washington					
Fairchild AFB		1			1
NH Bremerton		2			2
OCONUS					
Cambodia					
NAMRU-2	3	4	9	1	17
Country 2					
Location A		2			2
Japan					
Yokota AB		1			1
Kenya					
USAMRU-K	2	1	6		9
South Korea					
Brian Allgood ACH		1			1
Kunsan AB		1			1
Grand Total	**5**	**38**	**17**	**1**	**61**

The hemagglutinin (HA) gene from select influenza positives was sequenced using dye terminator, Sanger-based methods. Preliminary data are based on the sequence analysis of the hemagglutinin gene. Antigenic sites, receptor binding sites and glycosylation motifs are predicated upon correlations with previously published experimental evidence.[1,3,4] Sequence data was constructed and analyzed using multiple software programs. Genetic and predicted antigenic information that resulted from this analysis is shared with United States Centers for Disease Control and Prevention (CDC), World Health Organization (WHO) and contribute to the seasonal Northern and Southern Hemisphere vaccine component selections.

Influenza A(H1N1)pdm09

- Among the 43 influenza A isolates, five (11.6%) were influenza A(H1N1)pdm09. The influenza A(H1N1)pdm09 sequences are characterized in a neighbor-joining phylogenetic tree with reference strains rooted from the current vaccine strain, A/California/07/2009-like virus (Figure 3).
- The A(H1N1)pdm09 isolates characterized for this report exhibited an overall protein homology of 96.7%-97.1% (average 96.9%) compared to the 2016-2017 influenza vaccine component, A/California/07/2009-like virus.
- All of the A(H1N1)pdm09 HA sequences for this report contain mutations consistent with the predominating subgroup, referred to as group 6B. Three sequences from Cambodia classified as clade 6B.1 (distinguished by the mutations S162N and I216T) while the remaining two from Kenya classified as clade 6B only.
- Gain or loss of *N*-linked glycosylation sites has been shown to alter HA protein surface topology. A gain in glycosylation could be advantageous to the virus by virtue of a masking effect on important antibody recognition sites, thus potentially modulating viral antigenicity.[4] Observations are based solely on sequence motifs. For the influenza A(H1N1)pdm09 isolates characterized in this report, one mutation, S162N (serine to asparagine), was observed that could cause a gain of a glycosylation motif.
- Of the 21 mutations present in the A(H1N1)pdm09 isolates, nine occurred at predicted antigenic sites (zero at site A, two at site B, one at site C, three at site D, and three at site E) and one occurred at the receptor binding site.[2,5]

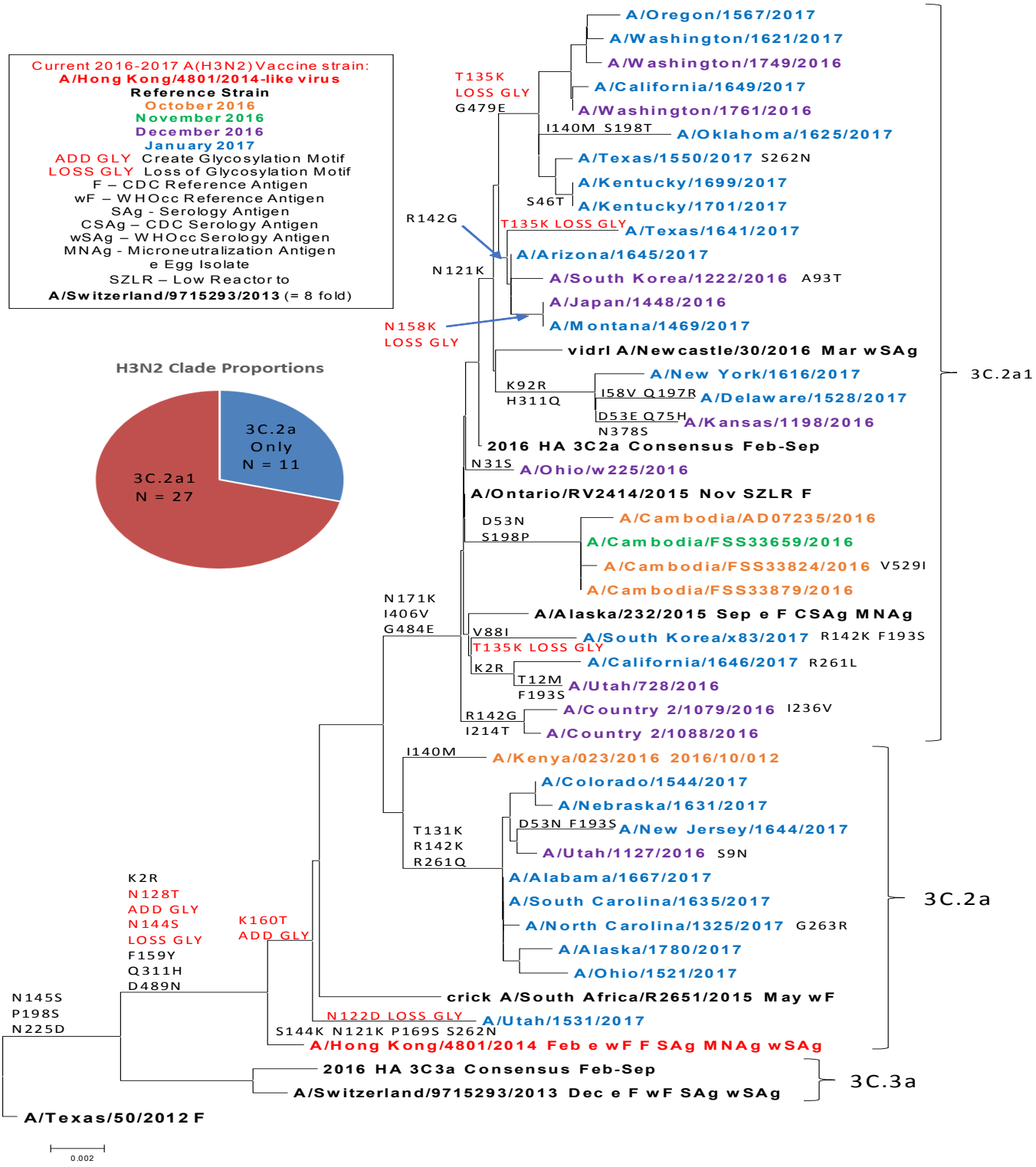
Figure 3: Influenza A(H1N1)pdm09 HA Phylogenetic Analysis



Influenza A(H3N2)

- Among the 43 influenza A isolates, 38 (88.4%) were influenza A(H3N2). The influenza A(H3N2) HA sequences are characterized in a neighbor-joining phylogenetic tree with reference strains rooted from a previous vaccine strain, A/Texas/50/2012 (Figure 4).
- The influenza A(H3N2) isolates characterized for this report exhibited an overall protein homology of 97.8%-99.3% (average 98.5%) compared to the 2016-2017 influenza vaccine component, A/Hong Kong/4801/2014-like virus.
- All of the influenza A(H3N2) isolates sequenced for this report were in clade 3C. All of the influenza A(H3N2) sequences classified as subclade 3C.2a and 27 (71.1%) further classified as the newly distinguished subclade within 3C.2a, 3C.2a1 (determined by the mutations N171K, I406V, and G484E). The mutation N121K was present in 17 (63.0%) of the 3C.2a1 isolates (44.7% of the total H3N2 isolates). Another mutation of interest, T135K, which has been suspected to infer viral protection[6], was present in 11 (40.7%) of the 3C.2a1 isolates (28.9% of the total H3N2 isolates) and 10 (58.8%) of the 3C.2a1 isolates also containing the mutation N121K. The combination of mutations R142G and I242V has also been suspected of providing viral protection, and while R142G was observed in this and previous reports, I242V was not.
- Among the influenza A(H3N2) isolates characterized in this report, four mutations; N122D (asparagine to aspartic acid), T135K (threonine to lysine), N144S (asparagine to serine), and N158K (asparagine to lysine) were observed that could cause the loss of a glycosylation motif. Two other mutations, N128T (asparagine to threonine) and K160T (lysine to threonine), were observed that could cause the gain of a glycosylation motif.
- Of the 42 mutations present in the A(H3N2) specimens, 15 occurred at predicted antigenic sites (five at site A, four at site B, one at site C, one at site D, and four at site E) and one occurred at the receptor binding site.[2,5]

Figure 4: Influenza A(H3N2) HA Phylogenetic Analysis



Influenza B

- The influenza B isolates are characterized in lineage specific, neighbor-joining phylogenetic trees with reference strains and are rooted from the reference strain B/Ohio/01/2005 for the B/Victoria isolates (Figure 5) and from the previous vaccine strain B/Massachusetts/02/2012-like virus for the B/ Yamagata isolates (Figure 6).
- The distinguishing characteristic between the two influenza B lineages (Victoria & Yamagata) is defined by an amino acid deletion in viruses belonging to the Yamagata lineage.[1] Seventeen (94.4%) of the influenza B isolates characterized in this report fell into the Victoria lineage and one (5.6%) fell into the Yamagata lineage.
- The influenza B/Victoria isolates characterized for this report exhibited a protein homology of 98.8% - 99.4% (average 99.2%) when compared to the 2016-2017 B/Victoria vaccine component, B/Brisbane/60/2008-like virus. (Note: due to truncated sequences in the data set, the first 33 bases (11 amino acids) and the last 276 bases (92 amino acids) were removed for this analysis, leaving a total of 1,449 bases (483 amino acids) for comparison.)
- The influenza B/Yamagata isolate characterized for this report exhibited a protein homology of 99.1% when compared to the 2016-2017 B/Yamagata vaccine component, B/Phuket/3073/2013-like virus.
- All of the influenza B/Victoria isolates fall into clade V1A and the B/Yamagata isolate falls into clade Y3. For the B/Victoria isolates, one mutation, A199T (alanine to threonine), adds a glycosylation motif. No changes in glycosylation were observed for the B/Yamagata isolate.
- Of interest, two of the influenza B/Victoria isolate sequences, both from Ft Bragg in North Carolina, contained a six base pair deletion causing a double amino acid deletion (positions 162-163), which falls in the same region as the single amino acid deletion at 162 observed in Yamagata lineage specimens. One B/Victoria sequence from Georgia, USA containing this deletion was previously reported by USAFSAM.

Figure 5: Influenza B/Victoria HA Phylogenetic Analysis

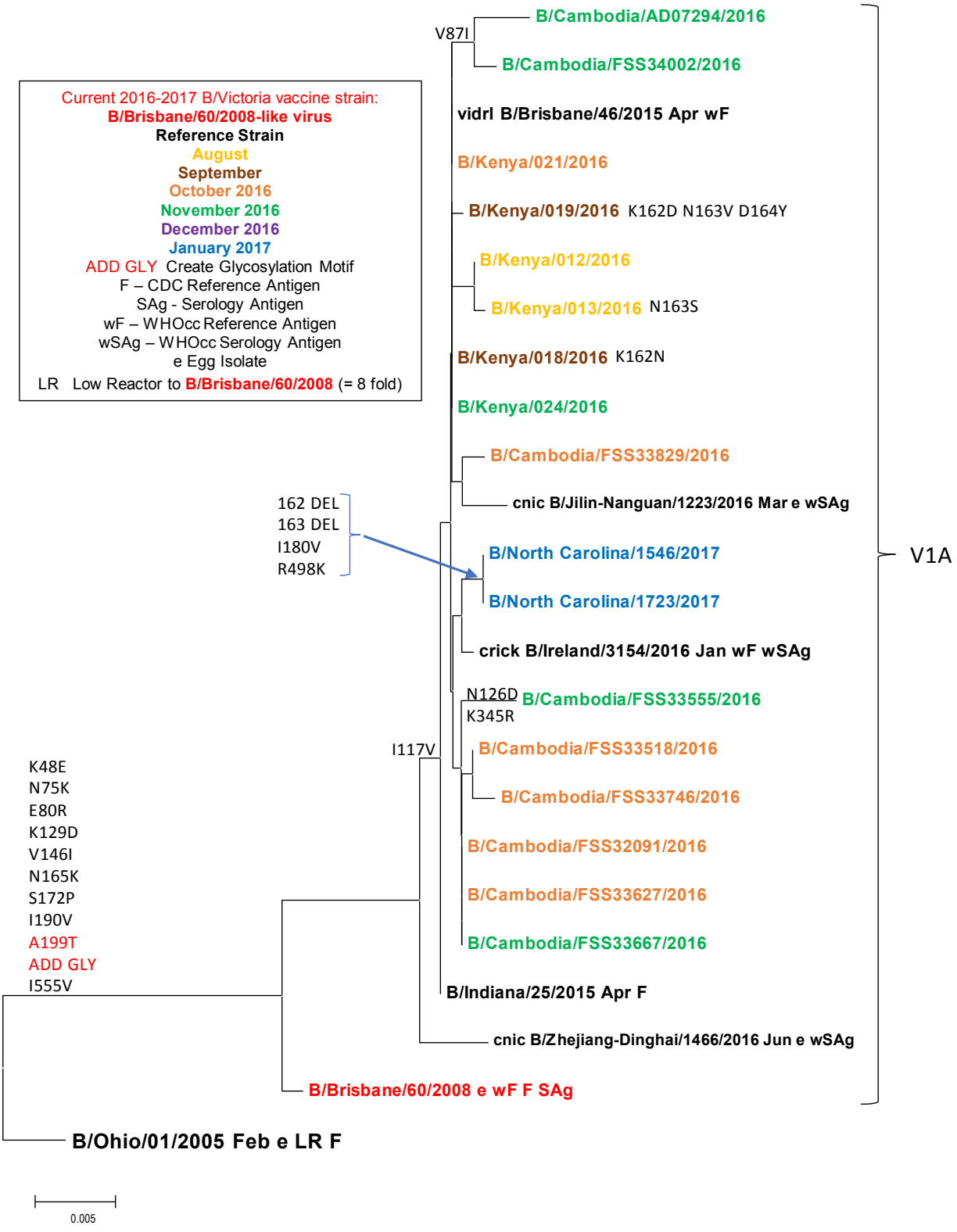
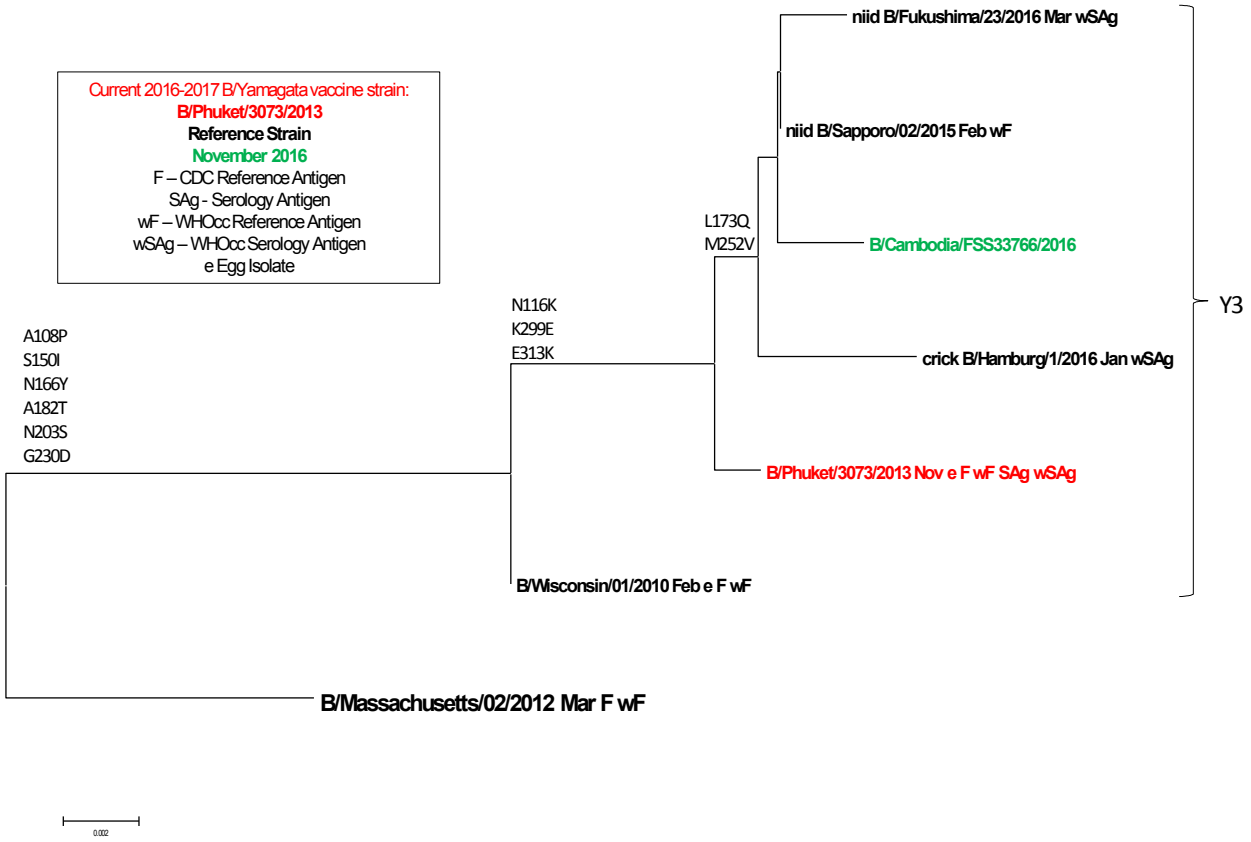


Figure 6: Influenza B/Yamagata HA Phylogenetic Analysis



References:

1. Wright, P., Neumann, G., and Kaqaoka, Y. (2007). Orthomyxoviruses In: Knipe, D.M., Howley, P.M. (Eds.), Fields Virology. Wolters Kluwer, Lippincott Williams & Wilkins, Philadelphia, pp.1692-1740.
2. Kongchanagul, A., Suptawiwat, O., Kanrai, P., Uiprasertkul, M., Puthavathana, P., and Auewarakul P. (2008). Positive selection at the receptor-binding site of hemagglutinin H5 in viral sequences derived from human tissues. Journal of Gen. Vir. **89**, 1805-1810.
3. Cherry, J.L., Lipman, D.J., Nikolskaya, A., and Wolf, Y.I. (2009). Evolutionary Dynamics of N-Glycosylation Sites of Influenza Virus Hemagglutinin. *PLoS Curr Influenza*. August 18: RRN1001.
4. Deem, M., and Pan, K. (2009). The epitope regions of H1-subtype influenza A, with application to vaccine efficacy. Protein Engineering, Design and Selection. **22**, no. 9. 543-546.
5. Wolf, Y.I., Viboud, C., Holmes, E.C., Koonin, E.V., and Lipman, D.J. (2006). Long intervals of stasis punctuated by bursts of positive selection in the seasonal evolution of influenza A virus. *Biol Direct*.; **1**: 34. doi: 10.1186/1745-6150-1-34.
6. Skowronski, D.M., Chambers, C., Sabaiduc, S., Dickinson, J.A., Winter, A., De Serres, G., Drews, S.J., Jassem, A., Gubbay, J.B., Charest, H., Balshaw, R., Bastien, N., Li, Y., and Krajden, M. (2017). Interim Estimates of 2016/17 Vaccine Effectiveness Against Influenza A(H3N2), Canada, January 2017. Eurosurveillance **22**, 6.

USAF School of Aerospace Medicine & Defense Health Agency

DoD Global, Laboratory-Based, Influenza Surveillance Program

Background

The DoD-wide program was established by the Global Emerging Infections Surveillance and Response System (GEIS) in 1997. The surveillance network includes the Defense Health Agency/Armed Forces Health Surveillance Branch—Air Force Satellite Cell (DHA/AFHSB-AF) and U.S. Air Force School of Aerospace Medicine (USAFSAM) (sentinel site respiratory surveillance), the Naval Health Research Center (recruit and shipboard population-based respiratory surveillance), the Naval Medical Research Unit (NAMRU-3) in Cairo, Egypt, the Naval Medical Research Unit (NAMRU-2) in Phnom Penh, Cambodia, the Armed Forces Research Institute of Medical Sciences (AFRIMS) in Bangkok, Thailand, the Naval Medical Research Unit (NAMRU-6) in Lima, Peru, and the United States Army Medical Research Unit-Kenya (USAMRU-K) located in Nairobi, Kenya. This work is supported by the Air Force and GEIS Operations, a Division of the Armed Forces Health Surveillance Branch (AFHSB).

Sentinel Site Surveillance

In 1976, the U.S. Air Force Medical Service began conducting routine, global, laboratory-based influenza surveillance. Air Force efforts expanded to DoD-wide in 1997. DHA/AFHSB-AF and USAFSAM manages the surveillance program that includes global surveillance among DoD beneficiaries at over 95 sentinel sites (including deployed locations) and many non-sentinel sites (please see map below). Collaborating partner laboratories include five DoD overseas medical research laboratories (AFRIMS, NAMRU-2, NAMRU-3, NAMRU-6, USAMRU-K) who collect specimens from local residents in surrounding countries that may not otherwise be covered in existing surveillance efforts. Additionally, the Naval Health Research Center (NHRC) in San Diego, CA collects specimens from DoD recruit training centers and conducts surveillance along the Mexico border.

Landstuhl Regional Medical Center (LRMC) and Tripler Army Medical Center (TAMC) assist the program by processing DoD specimens for the EUCOM region and the State of Hawaii, respectively. This process seeks to provide more timely results and efficient transport of specimens.

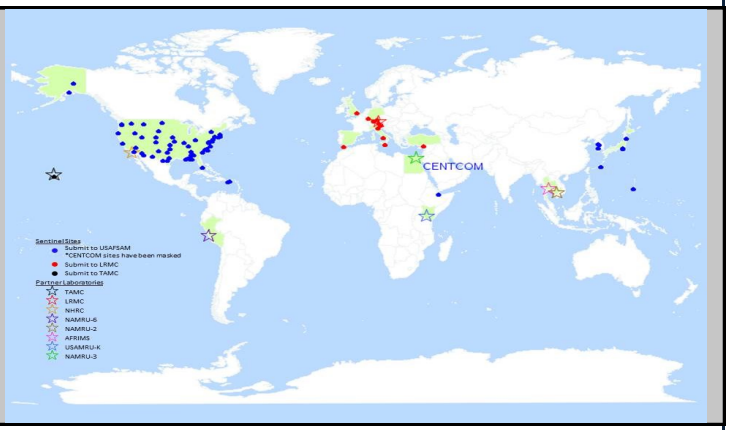
Available on our website (listed below) is a list of previous weekly surveillance reports, program information (including an educational briefing and instruction pamphlets for clinic staff), and a dashboard containing respiratory data for our sentinel sites.

Errata:

For Public Health Services
937-938-3196; DSN 798-3196

For Laboratory Services
937-938-4140; DSN 798-4140

USAFSAM.PHRFlu@us.af.mil



Collaborating Partners

In addition to all participating DoD military sentinel sites, collaborating laboratories and medical centers (described above) may be further understood by reviewing the sites' website. Click on the sites' icon to be directed to their webpage.

88ABW-2015-5508 and PA email guidance dated 10 November 2015.